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BLSA_HUMAN
MOES_LYTVA
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CYP8_CAEEL
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38.2% 35.4% vative	3071.1; B. 3;7 dstore_7 in; sign 586 586 69729	SIMILARITY: TO OTHER 7S SEED STORAGE CONVICILIN, CONGLYCININ, ETC.). SWISS-PROT entry is copyright. It is swiss Institute of Bioinfor European Bioinformatics Institute. Buropean Bioinformatics Institutions as lon by non-profit institutions as lonified and this statement is not removities requires a license agreement (Send an email to license@isb-sib.ch).	DM N.A. Pyle J.B., Legocki A real biochemistry of c al biochemistry of c XVIII. cDNA and ami protein families."; 3iol. 7:475-489(1986) N: SEED STORAGE PROTE JLAR LOCATION: COTYLE	ี ซีาำัก		708 743 1048 1336 321 321 386 386 386 386 388 614 505
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01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
VICILIN GC72-A PRECURSOR (ALPHA-GLOBULIN A).
MEDLINE=93280194;
                              SEQUENCE
                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
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                                                                                                                                                                                                                                                          TRICHOHYALIN.
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Plant Mol. Biol. 9:533-546(1987).
-:- FUNCTION: SEED STORAGE PROTEIN.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Malvales; Malvaceae; Gossypium.
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Developmental biochemistry of cottonseed embryogenesis and
Developmental biochemistry of cottonseed embryogenesis and
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Pred. No. 0.00
19; Mismatches
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; C9DB9371C976953B CRC64;
                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Steinert P
                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for content in the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                       INTERPRO; IPR001751; -. INTERPRO; IPR002048; -. PFAM; PF01023; S_100; 1.
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J. Invest. Dermatol. 101:65S-71S(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 envelope precursor, and
linking) protein.":
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                                                                                                                                                                                                       PROSITE; PS00018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED & SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAIN 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOLEGULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG DIFFERENT SPECIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIPRETIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK.
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TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES SITISTIES IN THE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA, AN THE FILLFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE) DEVELOPMENTAL STAGE: EXPRESSED DURING LATE DIFFERENTIATION OF THE EPIDERMIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
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                                                                                                                                                                                                                                                                                                                           A45973; A45973.
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                                                                                                                                                                    Calcium-binding.
                                                                                                                                                                                    PS00018; EF_HAND; 1.
PS00303; S100_CABP;
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Chem. 26
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                                                                                                                                                                                                                                                                                                                                                                           email to license@isb-sib.ch).
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                                                                                SITE I (LOW AFFINITY) (POTENTIAL).
SITE II (HICH AFFINITY) (POTENTIAL).
6 X 13 AA TANDEM REPEATS OF
R-R-E-Q-E-E-E-R-R-E-Q-Q-L.
                                                                                                                                                     S-100 LIKE
                               1 (APPROXIMATE).
2 (APPROXIMATE).
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CONFLICT
                                                                                   Fietz M.J., Rogers G.E.;

Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE GRANULAR LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY ISODIFIEDIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER
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01-OCT-2000
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                                                                                                                                                                     Mammalia;
                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit)
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               SUBUNIT: HOMODIMER (PROBABLE).
TISSUE SPECIFICITY: FOUND IN THE HARD KERATINIZING TISSUES S
THE INNER ROOT SHEAT (IRS) OF HAIR FOLLICLES AND MEDULLA, AN
THE FILIFORM PAPILLAE OF DORSAL TONGUE EPITHELIUM (PROBABLE)
                                                           WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CELL ENVELOPE OR EVEN ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED I ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINA
THE EPIDERMIS.
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23 X 26 AA APPROXIMATE TANDEM REPEATS.
F -> L (IN REF. 2).
QERDROYR -> RSETGSTG (IN REF. 2).
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-> G (IN REF. 2).
; A74B5947FB62E31D
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                                                                                                                                                                    Leporidae; Oryctolagus.
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30-MAY-2000
            separate domains are required for association with during interphase and with the central spindle duri J. Cell Biol. 123:373-385(1993).
                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                        Mackay A.M., Eckley D.M., Chue C., "Molecular analysis of the INCENPS
                                                                                  SEQUENCE FROM N.A. MEDLINE=94012983;
                                                                                                                                                   Archosauria;
                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
INNER CENTROMERE PROTEIN (INCENP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPR001751; -. INTERPRO; IPR002048; -. PFAM; PF01023; S_100; 1. PFAM; PF00036; efhand; 1
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-i- PIM: KNOWN SUBSTRATE OF TRANSGLUTAMINASE. SOME 200 ARGININES ARE
-PROBABLY CONVERTED TO CITRULLINES BY PEPTIDYLARGININE DEIMIDASE.
-i- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE S-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat; Calcium-binding.
DOMAIN 1 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00018; EF_HAND; 1. PROSITE; PS00303; S100_CABP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z19092; CAA79519.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                   314
                                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND CALCIUM-BINDING DOMAINS. DOMAINS 2-4, 6, AND 8 ARE ALMOST ENTIRELY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRANDED ALPHA-HELICAL ROD STABLILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS. DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
                                                                                                                                                                                                                                                                                                                                                                   EDEEKYEERMKE
                                                                                                                                                                                                                                                                                                                                                                                                          QQCRRECEETREREQRLEQEERREQ--QLRREQRLEQEERREQQCRRECEETREREQRL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                        QRDPQQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQK------RYEEQQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S28589; S28589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P02633; 1BOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                   Aves;
                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                        PubMed=8408220;
ey D.M., Chue C.,
                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183781 MW; AE17D2A159F12B7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S-100 LIKE.
SITE I (LOW AFFINITY) (POTENTIAL).
SITE II (HIGH AFFINITY) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                 Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100;
                                        (inner centromere proteins): association with microtubules
                                                                        Earnshaw W.C
                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                        877
                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
.21;
                                                                                                                                                                                                                                                                       ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Length 1407;
                                                                                                                                                Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                         during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                          anaphase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restrictions
                                                                                                                                              Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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L outstation -
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ACT AS CYTOSKELETAL PROTEINS THAT ARE POTENTIALLY

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UZR2_HUMAN
ID UZR2_H
AC Q15696
AC Q15696
DT 01-NOV
DT 15-DECV
DT 15-DECV
DE UZ SMA
DE RELATE
GN UZAP1--
OS HOMO S
OC EUKARY
OC MAMMAI
RN [1]
RN [1]
RN TISSUE
RX KITA99
RA KITA94
RA MIXA1
RA MIXA1
RT UZaf1-
RT UZaf1-
CC -!-SI
CC -!-SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Вb
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U2R2_HUMAN
Q15696;
01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                   U2AF1-RS2 OR U2AF1RS2.
HOmo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                              Genomics 30:257-263(1995).
                                                                                                                                                                                                      Kitagawa
                                                                                                                                                                                                                          MEDLINE=96163878;
                                                                                                                                                                                                                                                      TISSUE-BRAIN;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         RELATED-PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell division; Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z25419; CAA80906.1; -. EMBL; Z25420; CAA80907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                        U2af1-rs1.",
                                                                                                                            "Isolation and mapping
                                                                                                                                                                            Inazawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606
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SUBCELLULAR LOCATION: NUCLEAR. IS RESTRICTED TO THE NUCLEUS IN INTERPHASE, REMAINS TIGHTLY BOUND TO THE CHROMOSOMES UNTIL EARLY METAPHASE, AND DURING LATE METAPHASE GETS CONCENTRATED IN LINEAR ARRAYS THAT TRANSECT THE METAPHASE PLATE BETWEEN THE CHROMOSOMES.
AS ANAPHASE BEGINS TO MOVE TO THE SPINDLE MIDZONE WHERE IT IS INTIMATELY ASSOCIATED WITH THE BUNDLED MICROTUBULES. LATER IN ANAPHASE GETS CLOSELY ASSOCIATED WITH THE CELL CORTEX, AND BY TELOPHASE IS CONCENTRATED AT EACH SIDE OF THE MIDBODY IN THE INTERCELLULAR BRIDGE, WITH WHICH IT IS DISCARDED AFTER.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; INCENP I AND INCENP II (SHOWN HERE); ARE PRODUCTED BY ALTERNATIVE SPLICING.
  SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF
SIMILARITY: TO MAMMALIAN SPLICING FACTOR UZAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPABLE OF ALTERING THE MONETWORK DURING INTERPHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QERKKE 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EERMKE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDPQQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDE---EKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EMEUROPEAN BIOINFORMATICS INSTITUTE. There are no restroy by non-profit institutions as long as its content and the supplementaries of the content of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRRQDEEARKQKALQQEEEEERRHKELMQKKKEEEQERARKIAEQRQAEQEREKQLAAERE 665
                                                                                                                                                                          J., Abe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                              ×.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 877 AA;
                                                                                                                                                                       Abe T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERING THE MORPHOLOGY OF THE CELLULAR MICROTUBULE
                                                                                                                                                   d; PubMed=8586425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100940 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.6%;
33.3%;
                                                                                                                            of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 97.5; D
Pred. No. 0.22
L6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing.
COLLED COLL (POTENTIAL).
MISSING (IN ISOFORM INCENP I).
A -> T.
A -> T.
A -> Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coiled coil; Centromere; Mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFA703149F555352 CRC64;
                                                                                                                            homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                           Hominidae; Homo
                                                                                                                            of
                                                                                                                                                                       Nojima
Murata
       U2AF
                                                                                                                            an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 877
       (RRM)
F 35 K
                                                                                                                          imprinted
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                                                                                                                                                                       A.,
                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                35
     KDA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                KDA SUBUNIT
                                                                                                                                                                            Monden
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                                                                                                                            mouse gene
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RESULT
GLT_DROME
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28,
01-FEB-1994 (Rel. 28,
30-MAY-2000 (Rel. 39,
GLUTACTIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00076; rrm; 1.
PFAM; PF00642; zf-CCCH; 1.
PROSITE; PS50102; RRM; 1.
Nuclear protein; Ribonucleoprotein.
Nuclear protein; Ribonucleoprotein.
DOMAIN
46
49
POLY-C
                                                                                                                                MIM;
                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                 Olson P.F., Fessler L.I.,
                                                                                                                                                                                                                                                                           STRAIN-OREGON-R;
                                                                                                                                                                                                                                                                                                      Ephydroidea;
[1]
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                            GLT_DROME
P33438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                                                                                                                                                                                                                                      Fessler
                                                                                                                                                                                                                                                              MEDLINE=90214632;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D49677; BAA08533.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPR000504; -. INTERPRO; IPR000571; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 KRQE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
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                                                                                                                       CARBOXYLESTERASE/LIPASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRDPQQQYEQCQKRCQRRETEPRHMQICQQRCERRYEKEKRKQQKRYEEQQREDEEKYEE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300028;
X53286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
19; Conser
                                                                                                                                                                                                                                      J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                              Drosophilidae; Drosophila
CAA37380
                                                                                                                                                                                                                                                                                     N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                               PubMed-2108864;
                                                                                                                                                                                                                                                                                                                                                                                     28, Created)
28, Last sequence update)
39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 I
58044 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.5%;
                                                                                                                                                                                                                                                                                     PARTIAL SEQUENCE
                                                                                                                                                                                                                                                 Nelson R.E., Sterne R.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97; DB
Pred. No. 0.14
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1DACC8A6CA4727A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        1023
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                                                                      There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA
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                                    isb-sib.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SBP_SOYBN
Q04672;
Q1-JUN-1994
                                                                                 -!- FUNCTION: PLAYS A ROLE IN SUCROSE TRANSPORT.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED:
-!- TISSUE SPECIFICITY: ASSOCIATED WITH THE PLASMA MEMBRANE OF
SEVERAL CELL TYPES ENGAGED IN SUCROSE TRANSPORT, INCLUDING THE
MESOPHYLL CELLS OF YOUNG SINK LEAVES, THE COMPANION CELLS OF
MATURE PHLOEM AND THE CELLS OF DEVELOPING COTYLEDONS.
-!- DEVELOPMENTAL STAGE: IN THE COTYLEDON, EXPRESSION IS NOT DETECTED
UNTIL 10 DAYS AFTER FERTILIZATION. BETWEEN 10-19 DAYS AFTER
FERTILIZATION, EXPRESSION INCREASES RAPIDLY BUT DECLINES 20-30
DAYS AFTER FERTILIZATION. 30 DAYS AFTER FERTILIZATION, NO
EXPRESSION OCCURS. THIS EXPRESSION PATTERN CLOSELY PARALLELS THE
RATE OF SUCROSE UPTAKE IN THE COTYLEDON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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DISULFID
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CARBOHYD
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SIMILAR
                                                                                                                                                                                                                                                                                                                                              Eukaryota; viridiplantae; Embryophy
Magnoliophyta; eudicotyledons; core
Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                          "A 62-kD sucrose binding protein is expressed and tissues actively engaged in sucrose transport."; Plant Cell 4:1561-1574(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
Glycoprotein; Sulfatation; Calcium-binding;
                                                                                                                                                                                                                                                                                   Grimes H.D., Overvoorde P.J., Ripp K., Franceschi
                                                                                                                                                                                                                                                                                               MEDLINE=93104680; PubMed=1467654;
                                                                                                                                                                                                                                                                                                               TISSUE=EMBRYO;
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                                                                                                                                                                                                                                                                                                                                                                                        Glycine max (Soybean)
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FLYBASE; FBgn0001114; Glt.
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    Last sequence update)
    Last annotation update

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BY SIMILARITY.
MW; 3638CF79AE
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Pred. No. 0.
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POLY-THR.
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Best Local :
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P18480;
           between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      Holmstroem K., Brandt T., Kallesoe T.;
"The sequence of a 32,420 bp segment located on the r. chromosome II from Saccharomyces cerevisiae.";
Yeast 10:S47-S62(1994).
-!- FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-2090 (Rel. 40, Last annotation update
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWL/
(TRANSCRIPTION FACTOR TYE4).
                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                           "The SNF5 protein of Saccharomyces cerevisiae is a glutamine- and proline-rich transcriptional activator that affects expression of broad spectrum of genes.";
Mol. Cell. Biol. 10:5616-5625(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
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PFAM; PF00546; Seedstore_7s;
                                                                                                                                 -!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                   MEDLINE=94378722; PubMed=8091861;
                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91042489; PubMed=2233708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MCY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast)
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HSSP; P50477; 1CAW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Jaurent B.C., Treitel M.A., Carlson M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103
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                                                                                                                                                                             COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER OF GENES. THIS COMPLEX ALTERS CHROMATIN STRUCTURE TO FACILITATE BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS. SUBUNIT: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
                                                                                                                                                                COMPLEX
                                                                                   SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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cetaceae; Saccharomyces.
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RESULT
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Best Local Similarity 24.9
Matches 15; Conservative
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        P34099;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (EC 2.7.1.37)
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DOMAIN
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DOMAIN
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SGD;
                                                                                                                      Mann S.K.O., Yonemoto W.M., Taylor S.S., Firtel R.A.; "DdPK3, which plays essential roles during Dictyostelium develoencedes the catalytic subunit of cAMP-dependent protein kinase. Proc. Natl. Acad. Sci. U.S.A. 89:10701-10705(1992).
                                                                                                                                                                                                                               MEDLINE=93385090; pubMed=8373760;
Anjard C., Etchebehere L., Pinaud
"An unusual catalytic subunit for
of Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                     Buerki E., Anjard C., Scholder J.-C., Reymond C.D "Isolation of two genes encoding putative protein during pictyostelum discoideum development."; gene 102:57-65(1991).
                                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum (Slime mold)
Eukaryota; Dictyosteliida; Dictyostel
                                                                                                                                                                                                                                                                                                                                                                                                                PKAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KAPC
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                                                                                                                                                                                             CHARACTERIZATION
                                                                                                                                                                                                                    Biochemistry
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91323730;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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A MAXIMUM AT SIMILARITY: CAMP SUBFAMI
                                 FUNCTION: ESSENTIAL FOR DIFFERENTIATION AND FRUIT MORPHOGENESIS. CATALYTIC ACTIVITY: ATP + A PROTEIN = ADP + A PHOSPHOPROTEIN. SUBUNIT: IN DICTYOSTELIUM THE HOLOENZYME IS A DIMER COMPOSED OF A REGULATORY (R) AND A CATALYTIC (C) SUBUNIT. IN THE PRESENCE OF CAMP IT DISSOCIATES INTO THE ACTIVE C SUBUNIT AND AN R MONOMER. DEVELOPMENTAL STAGE: CAPK ACTIVITY IS LOW IN VEGETATIVELY GROWING AMOEBAE, INCREASES DURING DEVELOPMENT OF AGGREGATION AND REACHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S44551; RGBYS5.
S39145; S39145.
S0000493; SNF5.
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X76053; CAA53652.1;
Z36158; CAA85254.1;
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01-FEB-1996 (Rel. 33
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01-OCT-1996 (Rel. 34
HYPOTHETICAL 122.9 K
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Robmitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: TO YEAST YNLO91W.
This Swree-pro-
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BINDING 365
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           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                            Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycc
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                                                                                                                                                                                                                        SPAC29E6.10C
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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DICTYDB; DD02030; PKAC.
INTERPRO; IPR000719; -.
INTERPRO; IPR000961; -.
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33, Last sequence update)
34, Last annotation update)
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ATP (BY SIMILARITY).
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Hypothetical
DOMAIN
                                                         modified and this statement is not removed entitles requires a license agreement (See or send an email to license@ish-sih ah)
                                                                                                                                                            -!- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR COMPONENT OF HDL AND CHYLOMICRONS.
-!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- TISSUE SPECIFICITY: SECRETED IN PLASMA.
-!- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-HELICAL, AND MANY OF THESE HELICES ARE MAPHIPATHIC. THEY MAY THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
-!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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Biochim. Biophys. Acta 1172:335-339(1993).
        EMBL; X68361; CAA48421.1;
PIR; S29565; S29565.
PIR; S30195; S30195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence upda:
15-DEC-1998 (Rel. 37, Last annotation upo
APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P33621;
01-FEB-1994
                                                                                                              the European Bioinformatics Institute.
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Y192_HUMAN
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Q93074;
Q1-NOV-1997
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Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
"Prediction of the coding sequences of unidentified human genes.
The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced analysis of cDNA clones from human cell line KG-1.";
DNA Res. 3:17-24(1996).
-!- TISSUE SPECIFICITY: UBIQUITOUS.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROTEIN KIAAO192 (FRAGMENT).
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Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                     "A Caenorhabditis elegans prospero homologue defines a novel doma. Trends Biochem. Sci. 19:70-71(1994).
-i- FUNCTION: INVOLVED IN THE CONTROL OF OTHER NEURONAL PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY TO C.ELEGANS CEH-26. MEDLINE-94212446; PubMed-7909177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chu-Lagraff Q., Wright D.M., McNeil L.K., Doe C.Q.; "The prospero gene encodes a divergent homeodomain controls neuronal identity in Drosophila."; Development Suppl. 2:79-85(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsuzaki F., Kolzumi K., Hamma C., Matsuzaki F., Kolzumi K., Hamma C., Matsuzaki F., Kolzumi K., Hamma C., Matsuzaki F., Kolzumi K., Hamma K., Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92171948; PubMed=1540176; Matsuzaki F., Koizumi K., Hama C.,
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Vaessin H., Grell E., Wolff E., Bier E., Jan L.Y., Jan Y.N.;
"Prospero is expressed in neuronal precursors and encodes a
protein that is involved in the control of axonal outgrowth
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30-MAY-2000 (Rel. 39, Last ann
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                                   TRANSCRIPTION BY BINDING TO DNA.

SUBCELLULAR LOCATION: NUCLEAR.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; PROS-L (SHOWN HERE) AND PROS-S; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY HAVE DIFFERENT N-TERMINAL AMINO ACIDS OF THE HOMEODOMAIN.

TISSUE SPECIFICITY: NEURONAL PRECURSORS. EXPRESSED IN THE DEVELOPING CNS, LENS-SECRETING CONE CELLS OF THE BYE, AND MIDGIDEVELOPING CNS, LENS-SECRETING CONE CELLS OF THE BYE, AND MIDGIDEVELOPMENTAL STAGE: EXPRESSED IN NEURONAL PRECURSORS EARLY DUI
                                                                                                                                                                                                                                                                                 GENES AS WELL AS AXONAL OUTGROWTH AND PATHFINDING OF NUMEROUS CENTRAL AND PERIPHERAL NEURONS. IT IS PROBABLY GENERALLY REQUIRED FOR PROPER NEURONAL DIFFERENTIATION OF MOST OR ALL NEURONS & THEII PRECURSORS IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS, BUT NOT
  SIMILARITY:
                                                                                                                                                                                                                                                        FOR THE SPECIFICATION OF IDENTITY. PROSPERO PROTEIN MAY REGULATE
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15; Conser
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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BELONGS
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PROSPERO
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HOMEOBOX PROTEINS
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        Magnoliophyta; Liliopsida;
                            Zea mays (Maize)
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EMBL; D10609;
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                 Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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        Poales; Poaceae; Zea
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Best Local Similarity 33.3%;
Matches 22; Conservative 1
                                                                                                                                                                                                                                                                                                             CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWTSS-PROT entry is copyright. It is produced through a collaboration betwee, the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOCHEM. GENET. 27:239-251(1989).

11- PTM: THREE PROTEIN-PROCESSING STEPS OCCUR IN THE FORMATION OF THE MATURE PROTEIN FROM THE PRIMARY TRANSLATION PRODUCT.

11- POLYMORPHISM: THE THREE MOST COMMONLY OCCURRING GLB1 ALLELES HAVE THE DESIGNATION L, I, AND S FOR LARGE, INTERMEDIATE, AND SMALL PROTEINS, RESPECTIVELY.

11- SIMILARIT: TO OTHER 75 SEED STORAGE PROTEINS (PHASEOLIN, VICILIN, CONVICILIN, CONGLYCININ, ETC.).
                                                                                                                                                                                                                                                                                                                              PFAM; PF00546; Seedstore_7s; 1.
Seed storage protein; Signal.
SIGNAL 1 18 OR
PROPEP 19 86
CHAIN 87 573 GL(
CARBOHYD 349 349 N-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M24845; AAA33467.1; -. HSSP; P50477; 1CAW. MAIZEDB; 30181; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular characterization of the major maize embryo globulin encoded by the Glb1 gene."; plant Physiol. 91:636-643(1989).
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STRAIN=CV INBRED LINE VA26;
Belanger F.C., Kriz A.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPR001113; -.
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Pred. No. 0.47;
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